

89/869388

SEQUENCE LISTING

<110> Bates, Elizabeth
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<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND
 METHODS

<130> SF0977X

<140> 09/223,919

<141> 1998-12-31

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tggctctccc gtcccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174

Met Gly Arg Pro Leu Leu Leu

-19

-15

ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222

Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly

-10

-5

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tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270

Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys

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10

15

20

cac etc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc 318

His	Leu	Ser	Ala	Ser	Met	Gly	Gly	Ser	Val	Glu	Ile	Pro	Ile	Ser	Phe		
				25					30					35			
tat	tac	ccc	tgg	gag	tta	gcc	aca	gct	ccc	gac	gtg	aga	ata	tcc	tgg	366	
Tyr	Tyr	Pro	Trp	Glu	Leu	Ala	Thr	Ala	Pro	Asp	Val	Arg	Ile	Ser	Trp		
				40					45					50			
aga	cgg	ggc	cac	ttc	cac	ggg	cag	tcc	ttc	tac	agc	aca	agg	ccg	cct	414	
Arg	Arg	Gly	His	Phe	His	Gly	Gln	Ser	Phe	Tyr	Ser	Thr	Arg	Pro	Pro		
				55					60					65			
tcc	att	cac	aag	gat	tat	gtg	aac	cgg	ctc	ttt	ctg	aac	tgg	aca	gag	462	
Ser	Ile	His	Lys	Asp	Tyr	Val	Asn	Arg	Leu	Phe	Leu	Asn	Trp	Thr	Glu		
				70					75					80			
ggt	cag	aag	agc	ggc	ttc	ctc	agg	atc	tcc	aac	ctg	cag	aag	cag	gac	510	
Gly	Gln	Lys	Ser	Gly	Phe	Leu	Arg	Ile	Ser	Asn	Leu	Gln	Lys	Gln	Asp		
				85					90					95			100
cag	tct	gtg	tat	ttc	tgc	cga	gtt	gag	ctg	gac	aca	cgg	agc	tca	ggg	558	
Gln	Ser	Val	Tyr	Phe	Cys	Arg	Val	Glu	Leu	Asp	Thr	Arg	Ser	Ser	Gly		
				105					110					115			
agg	cag	cag	tgg	cag	tcc	atc	gag	ggg	acc	aaa	ctc	tcc	atc	acc	cag	606	
Arg	Gln	Gln	Trp	Gln	Ser	Ile	Glu	Gly	Thr	Lys	Leu	Ser	Ile	Thr	Gln		
				120					125					130			
gct	gtc	acg	acc	acc	acc	cag	agg	ccc	agc	agc	atg	act	acc	acc	tgg	654	
Ala	Val	Thr	Thr	Thr	Thr	Gln	Arg	Pro	Ser	Ser	Met	Thr	Thr	Thr	Trp		
				135					140					145			
agg	ctc	agt	agc	aca	acc	acc	aca	acc	ggc	ctc	agg	gtc	aca	cag	ggc	702	
Arg	Leu	Ser	Ser	Thr	Thr	Thr	Thr	Thr	Gly	Leu	Arg	Val	Thr	Gln	Gly		
				150					155					160			
aaa	cga	cgc	tca	gac	tct	tgg	cac	ata	agt	ctg	gag	act	gct	gtg	ggg	750	
Lys	Arg	Arg	Ser	Asp	Ser	Trp	His	Ile	Ser	Leu	Glu	Thr	Ala	Val	Gly		
				165					170					175			180
gtg	gca	gtg	gct	gtc	act	gtg	ctc	gga	atc	atg	att	ttg	gga	ctg	atc	798	
Val	Ala	Val	Ala	Val	Thr	Val	Leu	Gly	Ile	Met	Ile	Leu	Gly	Leu	Ile		
				185					190					195			
tgc	ctc	ctc	agg	tgg	agg	aga	agg	aaa	ggt	cag	cag	cgg	act	aaa	gcc	846	
Cys	Leu	Leu	Arg	Trp	Arg	Arg	Arg	Lys	Gly	Gln	Gln	Arg	Thr	Lys	Ala		
				200					205					210			
aca	acc	cca	gcc	agg	gaa	ccc	ttc	caa	aac	aca	gag	gag	cca	tat	gag	894	
Thr	Thr	Pro	Ala	Arg	Glu	Pro	Phe	Gln	Asn	Thr	Glu	Glu	Pro	Tyr	Glu		
				215					220					225			
aat	atc	agg	aat	gaa	gga	caa	aat	aca	gat	ccc	aag	cta	aat	ccc	aag	942	
Asn	Ile	Arg	Asn	Glu	Gly	Gln	Asn	Thr	Asp	Pro	Lys	Leu	Asn	Pro	Lys		
				230					235					240			

gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca 990
Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
245 250 255 260

ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag 1038
Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
265 270 275

acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa 1092
Thr Leu Tyr Ser Val Leu Lys Ala
280

tggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa gcctgaggca 1152
gaatcaagtg agcccaggag ttcagggcca gctttgataa tggagcgaga tgccatctct 1212
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Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
15 20 25
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
30 35 40 45
Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
50 55 60
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
65 70 75
Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
80 85 90
Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
95 100 105
Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
110 115 120 125
Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
130 135 140
Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr
145 150 155

Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser His Ile
 160 165 170
 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
 175 180 185
 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
 190 195 200 205
 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
 210 215 220
 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
 225 230 235
 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
 240 245 250
 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
 255 260 265
 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
 270 275 280

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 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg 168
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 -17 -15 -10 -5
 ctg ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca 216
 Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro
 1 5 10
 agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg 264
 Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met
 15 20 25

ggt ggc tct gtg gac ttc ccc ttc tcc ttc tat tac ccc ggc gag tta	312
Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu	
30 35 40	
gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac	360
Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His	
45 50 55 60	
ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat	408
Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr	
65 70 75	
gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc	456
Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe	
80 85 90	
ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc	504
Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys	
95 100 105	
cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc	552
Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser	
110 115 120	
atc gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa	600
Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys	
125 130 135 140	
gcc aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat	648
Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr	
145 150 155	
gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc	696
Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro	
160 165 170	
aag gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc	744
Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr	
175 180 185	
tca ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac	792
Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn	
190 195 200	
gag acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct	839
Glu Thr Leu Tyr Ser Val Leu Lys Ala	
205 210	
caagactgaa tgggtgaggcc aggtacagtg ggcacacct gtaatcccag ctactctgaa	899
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 20 25 30
 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
 35 40 45
 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60
 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75
 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
 80 85 90 95
 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 100 105 110
 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
 115 120 125
 Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr
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 Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile
 145 150 155
 Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
 160 165 170 175
 Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
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cagacatctg tgcctcattc ctgatctcaa ggggaaagca agaacaaggg aggcttcctc	180
aggatctcga acctgcggaa ggaggaccag tctgtgtact tctgccaaagt ccagctggac	240
atacagatca gggaggctgt cgtggcagtc catcaagggg acccacctca ccatcaccca	300
ggccctcagg cagcccctcc acagggcccc tctcctgcct ggacagctct gctggtctcc	360
ccgtccccctg gagaagaaca aggcc atg ggt cgg ccc ctg ctg ctg ccc ctg	412
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Leu Leu Leu Leu Gln Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr	
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gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa cac ctc	508
Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu	
10 15 20	
tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac	556
Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr	
25 30 35 40	
ccc tgg gag tta gcc ata gtt ccc aac gtg aga ata tcc tgg aga cgg	604
Pro Trp Glu Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg	
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ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct tcc att	652
Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile	
60 65 70	
cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag	700
His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln	
75 80 85	
gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct	748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser	
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gtg tat ttc tgc cga gtc gag ctg gac acc cgg aga tca ggg agg cag	796
Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln	
105 110 115 120	
cag ttg cag tcc atc aag ggg acc aaa ctc acc atc acc cag gct gtc	844
Gln Leu Gln Ser Ile Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val	
125 130 135	
aca acc acc acc acc tgg agg ccc agc agc aca acc acc ata gcc ggc	892
Thr Thr Thr Thr Thr Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly	
140 145 150	
ctc agg gtc aca gaa agc aaa ggg cac tca gaa tca tgg cac cta agt	940
Leu Arg Val Thr Glu Ser Lys Gly His Ser Glu Ser Trp His Leu Ser	
155 160 165	
ctg gac act gcc atc agg gtt gca ttg gct gtc gct gtg ctc aaa act	988
Leu Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr	
170 175 180	

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Leu Arg Val
160 165 170 175

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
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aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg ctg 171
Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu
-15 -10 -5

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Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
15 20 25

ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 315
Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
30 35 40 45

aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363
Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
50 55 60

cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 411
Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
65 70 75

aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459
Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
80 85 90

agg atc tcc aac ctt ag aag cag gac cag tct gtg tat c tgc cga 507
 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555
 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

gag ggg acc aaa ctc tcc atc acc cag ggg aac cct tcc aaa aca cag 603
 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
 130 135 140

agg agc cat atg aga ata tca gga atg aag gac aaa ata cag atc cca 651
 Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
 145 150 155

agc taa atcccaagga tgacggcatc gtctatgctt cccttgccct ctccagctcc 707
 Ser

acctcaccca gagcacctcc cagccaccgt cccctcaaga gccccagaa cgagaccctg 767

tactctgtct taaaggccta accaatggac agccctctca agactgaatg gtgaggccag 827

gtacagtggc gcacacctgt aatcccagct actctgaagc ctgaggcaga atcaagttag 887

cccaggagtt cagggccagc tt 909

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<212> PRT

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Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
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Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45

Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
 80 85 90

Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
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Ser

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 ataaaggaag tgctggtcac cctggaggtg tactggtttg gggaagggtcc ccggccccca 180
 cagccctctg gggagcctca ccctggetct cccactcac ctcagccctc aggcagcccc 240
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 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25
 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 494
 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45
 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 542
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60
 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 590
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75
 aac cgg ctc ttt ctg aac tgg aca gag ggt cag gag agc ggc ttc ctc 638
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
 80 85 90

agg atc tca aac ctg gg aag gag gac cag tct gtg tat c tgc cga 686
 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc 734
 Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
 110 115 120 125

aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc 782
 Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr
 130 135 140

tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa 830
 Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu
 145 150 155

agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc 878
 Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
 160 165 170

agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg 926
 Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu
 175 180 185

ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca 974
 Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro
 190 195 200 205

agc agt gac ttc tga ccaacagagt gtggggagaa gggatgtgta ttagccccgg
 1029
 Ser Ser Asp Phe

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